<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

<120> EXPRESSION SYSTEMS OF TOXIC PROTEINS, VECTORS
       AND PROCESS FOR MANUFACTURING TOXIC PROTEINS

<130> B14143 EE

<140>
<141>

<150> FR N°02 11676
<151> 2002-09-20

<160> 53

<170> PatentIn Ver. 2.1

<210> 1
<211> 37
<212> PRT
<213> Hepatitis C virus

<400> 1
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Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu Leu Phe
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Ala Gly Val Asp Ala
            35

<210> 2
<211> 31
<212> PRT
<213> Hepatitis C virus

<400> 2
Met Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val
 1   5   10   15

Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala
            20   25   30

<210> 3
<211> 111
<212> DNA
<213> Hepatitis C virus

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aactgggcta aagttctggt tgttctgctg ctgttcgctg gtgttgacgc t   111

<210> 4
<211> 93
<212> DNA
<213> Hepatitis C virus

<400> 4
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tggatgatgc tgctgatctc tcaggctgaa gct   93

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<210> 5
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide (+) of insertion into pT7-7

<400> 5
gggaatgcca tatgatcgct ggtg                                    24


<210> 6
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
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<400> 6
gcatatcgat ctaagcgtca aca                                     23


<210> 7
<211> 131
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: TME1 coding sens DNA
      + 3' cla I site

<400> 7
atgccatatg atcgctggtg ctcactgggg tgttctggct ggtatcgctt acttctctat 60
ggttggtaac tgggctaaag ttctggttgt tctgctgctg ttcgctggtg ttgacgctta 120
gatcgatatg c                                                 131


<210> 8
<211> 131
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: anticodant sens DNA
      + 5' cla I site

<400> 8
gcatatcgat ctaagcgtca acaccagcga acagcagcag aacaaccaga actttagccc 60
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tcatatggca t                                                 131


<210> 9
<211> 74
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      coding sens oligonucleotide for the synthesis of
      TME1

<400> 9
atgccatatg atcgctggtg ctcactgggg tgttctggct ggtatcgctt acttctctat 60
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ggttggtaac tggg   74

<210> 10
<211> 79
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
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      TME1

<400> 10
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agttaccaac catagagaa   79

<210> 11
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide (+) of insertion into pGEXKT without
      the dp site

<400> 11
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<210> 12
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide (+) of insertion into pGEXKT with
      the dp site

<400> 12
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<210> 13
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
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<400> 13
gaattcctaa gcttcagcct gag   23

<210> 14
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
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<400> 14
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<210> 15
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
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<400> 15
cgcatatgga cccgatcgct ggtgct   26

<210> 16
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
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<400> 16
gaattcctaa gcgtcaacac cagc   24

<210> 17
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
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<400> 17
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<210> 18
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
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<400> 18
aagcttaagc ttcagcctga gagatcag   28

<210> 19
<211> 103
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: sens DNA
      coding TME2 + 5' Nde I site and 3' Hind III site

<400> 19
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ctgtggatga tgctgctgat ctctcaggct gaagcttaag ctt   103

<210> 20
<211> 103
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: sens DNA
      anticoding TME2 + 3' Nde I site and 5' Hind III site

<400> 20
aagcttaagc ttcagcctga gagatcagca gcatcatcca caggcaagag caaacacgag 60
cgtcagccag cagcaggaac agcagaacaa cgtattccat atg   103

<210> 21
<211> 68
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      sens oligonucleotide (+) coding for the synthesis
      of TME2

<400> 21
catatggaat acgttgttct gctgttcctg ctgctggctg acgctcgtgt ttgctcttgc 60
ctgtggat   68

<210> 22
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      sens oligonucleotide (-) coding for the synthesis
      of TME2

<400> 22
aagcttaagc ttcagcctga gagatcagca gcatcatcca caggcaagac gaaacac   57

<210> 23
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide (+) of insertion into pGEXKT without
      the dp site

<400> 23
ggatccgaat acgttgttc   19

<210> 24
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide (+) of insertion into pGEXKT with
      the dp site

<400> 24
ggatccgacc cggaatacgt tgttc   25

<210> 25
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide (-) of insertion into pGEXKT with
      the dp site

<400> 25
gaattcttaa gcttcagcct gagagatcag   30

<210> 26
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide (+) of insertion into pT7-7

<400> 26
cgcatatgga cccggaatac gttgttc   27

<210> 27
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide (-) of insertion into pT7-7

<400> 27
cagaattcct aagcttcagc ctgagag   27

<210> 28
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: end of the
      GST followed by the thrombine site

<400> 28
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 1   5   10   15

<210> 29
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: DNA
      coding for GST protein in the pGEXKT vector

<400> 29
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<210> 30
<211> 327
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: DNA
      coding for the thioredoxine in the pET32a+ vector

<400> 30
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atcgatcaaa accctggcac tgcgccgaaa tatggcatcc gtggtatccc gactctgctg 240
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aaagagttcc tcgacgctaa cctggcc 327

<210> 31
<211> 4969
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: plasmide
      expressing pGEXKT

<400> 31
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<210> 32
<211> 11800
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: plasmide
      expressing pET32a+

<400> 32
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<210> 33
<211> 2504
<212> DNA

<213> Artificial sequence

<220>
<223> Description of the artificial sequence: plasmide
        expressing pT7-7

<400> 33
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<210> 34
<211> 813
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression system
        coding for fusion protein GST-DP-TME1

<400> 34
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gatattagat acggtgtttc gagaattgca tatagtaaag actttgaaac tctcaaagtt 360
gattttctta gcaagctacc tgaaatgctg aaaatgttcg aagatcgttt atgtcataaa 420
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tggggtgttc tggctggtat cgcttacttc tctatggttg gtaactgggc taaagttctg 780
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<210> 35
<211> 513
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression system
      coding for fusion protein TrX-DP-TME1

<400> 35
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ccgattctgg atgaaatcgc tgacgaatat cagggcaaac tgaccgttgc aaaactgaac 180
atcgatcaaa accctggcac tgcgccgaaa tatggcatcc gtggtatccc gactctgctg 240
ctgttcaaaa acggtgaagt ggcggcaacc aaagtgggtg cactgtctaa aggtcagttg 300
aaagagttcc tcgacgctaa cctggccggt tctggttctg gatctccaaa atcggatctg 360
tctggtggtg gtggtggtct ggttccgcgt ggatccgacc cgatcgctgg tgctcactgg 420
ggtgttctgg ctggtatcgc ttacttctct atggttggta ctgggctaa agttctggtt 480
gttctgctgc tgttcgctgg tgttgacgct tag                             513
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<210> 36
<211> 117
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression system
      coding for fusion protein M-DP-TME1

<400> 36
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atggacccga tcgctggtgc tcactggggt gttctggctg gtatcgctta cttctctatg 60
gttggtaact gggctaaagt tctggttgtt ctgctgctgt tcgctggtgt tgacgct   117
```

<210> 37
<211> 795
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression system
      coding for fusion protein
      GST-DP-TME2

<400> 37
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atgtcccta tactaggtta ttggaaaatt aagggccttg tgcaacccac tcgacttctt 60
ttggaatatc ttgaagaaaa atatgaagag catttgtatg agcgcgatga aggtgataaa 120
tggcgaaaca aaaagtttga attgggtttg gagtttccca atcttcctta ttatattgat 180
ggtgatgtta aattaacaca gtctatggcc atcatacgtt atatagctga caagcacaac 240
atgttgggtg gttgtccaaa agagcgtgca gagatttcaa tgcttgaagg agcggttttg 300
gatattagat acggtgtttc gagaattgca tatagtaaag actttgaaac tctcaaagtt 360
gattttctta gcaagctacc tgaaatgctg aaaatgttcg aagatcgttt atgtcataaa 420
acatatttaa atggtgatca tgtaacccat cctgacttca tgttgtatga cgctcttgat 480
gttgttttat acatggaccc aatgtgcctg gatgcgttcc caaaattagt ttgtttttaaa 540
aaacgtattg aagctatccc acaaattgat aagtacttga aatccagcaa gtatatagca 600
tggcctttgc agggctggca agccacgttt ggtggtggcg accatcctcc aaaatcggat 660
ctgtctggtg gtggtggtgg tctggttccg cgtggatccg acccggaata cgttgttctg 720
ctgttcctgc tgctggctga cgctcgtgtt tgctcttgcc tgtggatgat gctgctgatc 780
```

tctcaggctg aagct

<210> 38
<211> 486
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression system
     coding for fusion protein
 TrX-DP-TME2

<400> 38
atgagcgata aaattattca cctgactgac gacagttttg acacggatgt actcaaagcg 60
gacggggcga tcctcgtcga tttctgggca gagtggtgcg gtccgtgcaa aatgatcgcc 120
ccgattctgg atgaaatcgc tgacgaatat cagggcaaac tgaccgttgc aaaactgaac 180
atcgatcaaa accctggcac tgcgccgaaa tatggcatcc gtggtatccc gactctgctg 240
ctgttcaaaa acggtgaagt ggcggcaacc aaagtgggtg cactgtctaa aggtcagttg 300
aaagagttcc tcgacgctaa cctggccggt tctggttctg gatctgatct gtctggtggt 360
ggtggtggtc tggttccgcg tggatccgac ccggaatacg ttgttctgct gttcctgctg 420
ctggctgacg ctcgtgtttg ctcttgcctg tggatgatgc tgctgatctc tcaggctgaa 480
gcttag 486

<210> 39
<211> 99
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression system
     coding for fusion protein M-DP-TME2

<400> 39
atggacccgg aatacgttgt tctgctgttc ctgctgctgg ctgacgctcg tgtttgctct 60
tgcctgtgga tgatgctgct gatctctcag ctgaagct 99

<210> 40
<211> 5082
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression vector
     pGEXKT-dp-Pt(TME1)

<400> 40
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tctggataat gttttttgcg ccgacatcat aacggttctg gcaaatattc tgaaatgagc 180
tgttgacaat taatcatcgg ctcgtataat gtgtggaatt gtgagcggat aacaatttca 240
cacaggaaac agtattcatg tcccctatac taggttattg gaaaattaag ggccttgtgc 300
aacccactcg acttcttttg gaatatcttg aagaaaaata tgaagagcat ttgtatgagc 360
gcgatgaagg tgataaatgg cgaaacaaaa agtttgaatt gggtttggag tttcccaatc 420
ttccttatta tattgatggt gatgttaaat taacacagtc tatggccatc atacgttata 480
tagctgacaa gcacaacatg ttgggtggtt gtccaaaaga gcgtgcagag atttcaatgc 540
ttgaaggagc ggttttggat attagatacg tgtttcgag aattgcatat agtaaagact 600
ttgaaactct caaagttgat tttcttagca agctacctga atgctgaaa atgttcgaag 660
atcgtttatg tcataaaaca tatttaaatg gtgatcatgt aacccatcct gacttcatgt 720
tgtatgacgc tcttgatgtt gtttatacaa tggacccaat gtgcctggat gcgttcccaa 780
aattagtttg ttttaaaaaa cgtattgaag ctatcccaca aattgataag tacttgaaat 840
ccagcaagta tatagcatgg cctttgcagg ctggcaagc acgtttggt ggtggcgacc 900
atcctccaaa atcggatctg tctggtggtg tggtggtct ggttccgcgt ggatccgacc 960
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tcgtgactga ctgacgatct gcctcgcgcg tttcggtgat gacggtgaaa acctctgaca 1140

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catgcagctc ccggagacgg tcacagcttg tctgtaagcg gatgccggga gcagacaagc 1200
ccgtcagggc gcgtcagcgg gtgttggcgg gtgtcggggc gcagccatga cccagtcacg 1260
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tgtgcgcgga acccctattt gtttattttt ctaaatacat tcaaatatgt atccgctcat 1440
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accagtcaca gaaaagcatc ttacggatgg catgacagta agagaattat gcagtgctgc 1860
cataaccatg agtgataaca ctgcggccaa cttacttctg acaacgatcg gaggaccgaa 1920
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cccacggaga atccgacggg ttgttactcg ctcacattta atgttgatga aagctggcta 5040
caggaaggcc agacgcgaat tattttttgat ggcgttggaa tt                    5082
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<210> 41
<211> 5064
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression vector
     pGEXKT-dp-Pt(TME2)

<400> 41
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gtatggctgt gcaggtcgta aatcactgca taattcgtgt cgctcaaggc gcactcccgt 120
tctggataat gttttttgcg ccgacatcat aacggttctg gcaaatattc tgaaatgagc 180
tgttgacaat taatcatcgg ctcgtataat gtgtggaatt gtgagcggat aacaatttca 240
cacaggaaac agtattcatg tcccctatac taggttattg gaaaattaag ggccttgtgc 300
aacccactcg acttcttttg gaatatcttg aagaaaaata tgaagagcat ttgtatgagc 360
gcgatgaagg tgataaatgg cgaaacaaaa agtttgaatt gggtttggag tttcccaatc 420
ttccttatta tattgatggt gatgttaaat taacacagtc tatggccatc atacgttata 480
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<210> 42
<211> 5918
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression vector
      pET32a-dp-Pt(TME1)

<400> 42
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tgttagcagc cggatctcag tggtggtggt ggtggtgctc gagtgcggcc gcaagcttgt 180
cgacggagct cgaattccta agcgtcaaca ccagcgaaca gcagcagaac aaccagaact 240
ttagcccagt taccaaccat agagaagtaa gcgataccag ccagaacacc ccagtgagca 300
ccagcgatcg ggtcggatcc acgcggaacc agaccaccac caccaccaga cagatccgat 360
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<212> DNA
<213> Artificial sequence

<220>
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<212> DNA
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<220>
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ataacactgc ggccaactta cttctgacaa cgatcggagg accgaaggag ctaaccgctt 2160
ttttgcacaa catgggggat catgtaactc gccttgatcg ttgggaaccg gagctgaatg 2220
aagccatacc aaacgacgag cgtgacacca cgatgcctgt agcaatggca caacgttgc 2280
gcaaactatt aactggcgaa ctacttactc tagcttcccg gcaacaatta atagactgga 2340
tggaggcgga taaagttgca ggaccacttc tgcgctcggc ccttccggct ggctggttta 2400
ttgctgataa atctggagcc ggtgagcgtg ggtctcgcgg tatcattgca gcactgggGc 2460
cagatggtaa gccctcccgt atcgtagtta tctacacgac ggggagtcag gcaactatgg 2520
atgaacgaaa tagacagatc gctgagatag gtgcctcact gattaagcat tggtaactgt 2580
cagaccaagt ttactcatat atactttaga ttgattt                            2617
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<210> 45
<211> 2599
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression vector
      pT7-7-dp-Pt(TME2)

<400> 45
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caagagcaaa cacgagcgtc agccagcagc aggaacagca gaacaacgta ttccgggtcc 180
atatgtatat ctccttctta aagttaaaca aaattatttc tagagggaaa ccgttgtggt 240
ctccctatag tgagtcgtat taatttcgaa gtctatcaga agttcgaatc gctgggcctc 300
gcgcgtttcg gtgatgacgg tgaaaacctc tgacacatgc agctcccgga cacggtcaca 360
gcttgtctgt aagcggatgc cgggagcaga caagcccgtc agggcgcgtc agcgggtgtt 420
ggcgggtgtc ggggcgcagc catgacccag tcacgtagcg atagcggagt gtatatactg 480
gcttaactat gcggcatcag agcagattgt actgagagtg caccatagga agatcttccg 540
gaagatcttc ctatgcggtg tgaaataccg cacagatgcg taaggagaaa ataccgcatc 600
aggcgctctt ccgcttcctc gctcactgac tcgctgcgct cggtcgttcg gctgcggcga 660
gcggtatcag ctcactcaaa ggcggtaata cggttatcca gaatcagg ggataacgca 720
ggaaagaaca tgtgagcaaa aggccagcaa aaggccagga accgtaaaaa ggccgcgttg 780
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tccggtaact atcgtcttga gtccaacccg gtaagacacg acttatcgcc actggcagca 1140
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tggtggccta actacggcta cactagaagg acagtatttg gtatctgcgc tctgctgaag 1260
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agcggtggtt tttttgtttg caagcagcag attacgcgca gaaaaaaagg atctcaagaa 1380
```
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```
gatcctttga tcttttctac ggggtctgac gctcagtgga acgaaaactc acgttaaggg 1440
attttggtca tgagattatc aaaaaggatc ttcacctaga tccttttaat tcttgaagac 1500
gaaagggcct cgtgatacgc ctattttat aggttaatgt catgataata atggtttctt 1560
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agcgtgacac cacgatgcct gtagcaatgg caacaacgtt gcgcaaacta ttaactggcg 2280
aactacttac tctagcttcc cggcaacaat taatagactg gatggaggcg gataaagttg 2340
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```

<210> 46
<211> 271
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
     GST-DP-TME1

<400> 46
```
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1               5                  10                  15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
     50                  55                  60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65                  70                  75                  80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                 85                  90                  95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130                 135                 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190
```

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195   200   205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly
    210   215   220

Gly Gly Gly Leu Val Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His
225   230   235   240

Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp
            245   250   255

Ala Lys Val Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
            260   265   270

<210> 47
<211> 265
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
      GST-DP-TME2

<400> 47
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
  1   5   10   15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20   25   30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
            35   40   45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50   55   60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65   70   75   80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85   90   95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100   105   110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115   120   125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130   135   140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145   150   155   160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165   170   175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180   185   190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195   200   205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly
    210   215   220

```
Gly Gly Gly Leu Val Pro Arg Gly Ser Asp Pro Glu Tyr Val Val Leu
225             230             235             240

Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys Ser Cys Leu Trp Met
                245             250             255

Met Leu Leu Ile Ser Gln Ala Glu Ala
                260             265
```

<210> 48
<211> 170
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
      TrX-DP-TME1

<400> 48
```
Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
  1             5              10             15

Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
            20             25             30

Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
            35             40             45

Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
    50             55             60

Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
 65             70             75             80

Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
                85             90             95

Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
            100            105            110

Ser Gly Ser Pro Lys Ser Asp Leu Ser Gly Gly Gly Gly Leu Val
            115            120            125

Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala
    130            135            140

Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val
145            150            155            160

Val Leu Leu Leu Phe Ala Gly Val Asp Ala
                165            170
```

<210> 49
<211> 161
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
      TrX-DP-TME2

<400> 49
```
Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
  1             5              10             15
```

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```
Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
          20              25              30

Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
          35              40              45

Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
    50              55              60

Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
65              70              75              80

Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
            85              90              95

Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
          100             105             110

Ser Gly Ser Asp Leu Ser Gly Gly Gly Gly Leu Val Pro Arg Gly
          115             120             125

Ser Asp Pro Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala
    130             135             140

Arg Val Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu
145             150             155             160

Ala
```

```
<210> 50
<211> 39
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
      M-DP-TME1

<400> 50
Met Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala
1               5               10              15

Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu
            20              25              30

Leu Phe Ala Gly Val Asp Ala
            35
```

```
<210> 51
<211> 33
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
      M-DP-TME2

<400> 51
Met Asp Pro Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala
1               5               10              15

Arg Val Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu
            20              25              30

Ala
```

<210> 52
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      glutathion transferase (GST)

<400> 52
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1   5   10   15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20   25   30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
            35   40   45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
        50   55   60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65   70   75   80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85   90   95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100   105   110 ·

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115   120   125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130   135   140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145   150   155   160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165   170   175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180   185   190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      · 195   200   205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly
    210   215   220

Gly Gly Gly Leu Val Pro Arg Gly Ser Pro Gly Ile His Arg Asp
225   230   235

<210> 53
<211> 170
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      thioredoxine (TrX)

<400> 53

```
Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
1               5                   10                  15

Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
            20                  25                  30

Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
            35                  40                  45

Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
        50                  55                  60

Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
65                  70                  75                  80

Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
                85                  90                  95

Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
            100                 105                 110

Ser Gly Ser Pro Lys Ser Asp Leu Ser Gly Gly Gly Gly Gly Leu Val
            115                 120                 125

Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala
        130                 135                 140

Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val
145                 150                 155                 160

Val Leu Leu Leu Phe Ala Gly Val Asp Ala
                165                 170
```